

score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

## OM nucleic - nucleic search, using sw model

(without alignments)  
8025.885 Million cell updates/sec

Sequence: 1 ccgcaatgacgcgcagcac...cgctagccttgtcagcg 559

Gapop 10.0 , Gapext 1.0

```
Searched:      2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280
```

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Genre1: \*

1: gb\_ba: \*

2: gb\_hg: \*

3: gb\_in: \*

4: gb\_om: \*

5: gb\_ov: \*

6: gb\_pat: \*

7: gb\_ph: \*

8: gb\_pl: \*

9: gb\_pr: \*

10: gb\_ro: \*

11: gb\_sts: \*

12: gb\_sy: \*

13: gb\_un: \*

14: gb\_vt: \*

15: en\_ba: \*

16: en\_fun: \*

17: en\_hum: \*

18: en\_in: \*

19: en\_mn: \*

20: en\_om: \*

21: en\_or: \*

22: en\_ov: \*

23: en\_pat: \*

24: en\_ph: \*

25: en\_pl: \*

26: en\_ro: \*

27: en\_sts: \*

28: en\_un: \*

29: en\_vt: \*

30: en\_hg\_hum: \*

31: en\_hg\_in: \*

32: en\_hg\_om: \*

33: en\_hg\_mus: \*

34: en\_hg\_pln: \*

35: en\_hg\_prod: \*

36: en\_hg\_man: \*

37: en\_hg\_vrt: \*

38: en\_sy: \*

39: en\_hg\_hum: \*

40: en\_hg\_mus: \*

41: en\_hg\_om: \*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB	ID	Description
1	559	100.0	559	6	AR073589	AR073589 Sequence
2	559	100.0	1583	6	AX400036	AX400036 Sequence
3	436.2	78.0	1679	9	AK093402	AK093402 Homo sapi
4	435.4	77.9	1726	9	AK094084	AK094084 Homo sapi
5	431.4	77.2	1432	9	AK056965	AK056965 Homo sapi
6	425.2	76.1	1835	9	BC019324	BC019324 Homo sapi
7	425.2	76.1	1835	9	BC019324	BC019324 Homo sapi
8	122.4	21.9	189149	2	AC046171	AC046171 Homo sapi
9	122.4	21.9	194567	2	AC055866	AC055866 Homo sapi
10	113.8	20.4	189149	2	AC046171	AC046171 Homo sapi
11	103	18.4	782	9	HMPERA	L24804 Human (p23)
12	103	18.4	1490	9	BC003005	BC003005 Homo sapi
13	103	18.4	3342	9	AK057820	AK057820 Homo s
14	101.8	18.2	2928	9	AK098214	AK098214 Homo s
15	101.4	18.1	127436	6	AC104459	AC104459 Homo sapi
16	101.2	18.1	483	6	BD012892	BD012892 Protein h
17	101.2	18.1	483	23	BD008327	BD008327 Protein h
18	96.4	17.2	1208	10	BC003708	BC003708 Mus muscu
19	96.4	17.2	1510	10	AB024935	AB024935 Mus muscu
20	94.6	16.9	483	10	AF153479	AF153479 Mus muscu
21	94.4	16.9	84558	2	AC123346	AC123346 Rattus no
22	93.4	16.7	134004	9	AC079768	AC079768 Homo sapi
23	93.4	16.7	135342	9	AC106878	AC106878 Homo sapi
24	93	16.6	570	6	AX341269	AX341269 Sequence
25	90.4	16.2	79302	2	AC023898	AC023898 Mus muscu
26	90.4	16.2	139242	10	AL590996	AL590996 Mouse DNA
27	84.8	15.2	468	5	CHKPGORC	L24898 Gallus gall
28	83.4	14.9	126452	2	AC118313	AC118313 Rattus no
29	83.4	14.9	146996	2	AC116195	AC116195 Rattus no
30	80.4	14.4	221184	2	AL733315	AL733315 Mus muscu
31	75.4	13.5	3455	9	HSZNF	X56465 Human znf6
32	75.2	13.5	473	6	AX440283	AX440283 Sequence
33	56.6	10.1	1776	6	AX364853	AX364853 Sequence
34	54.2	9.7	138928	9	AC068487	AC068487 Homo sapi
35	54.2	9.7	179599	9	AC013278	AC013278 Homo sapi
36	53.8	9.6	117753	9	AL358789	AL358789 Homo sapi
37	53.8	9.6	173758	9	AC008144	AC008144 Human DNA
38	46.6	8.3	124557	9	AL390834	AL390834 Homo sapi
39	46.6	8.3	160737	2	AC026213	AC026213 Homo sapi
40	46.6	8.3	191064	2	AL161745	AL161745 Homo sapi
41	46.6	8.3	203722	2	AC026195	AC026195 Homo sapi
42	43.4	7.8	137329	2	AC095733	AC095733 Rattus no
43	43.4	7.8	200289	2	AC090681	AC090681 Homo sapi
44	43.4	7.8	202235	2	AC117378	AC117378 Homo sapi
45	42	7.5	7218	6	166494	Sequence 14

RESULT 1				
AR073589				
LOCUS	AR073589	559 bp	DNA	linear
DEFINITION	Sequence 2 from patent US 5952175.			
ACCESSION	AR073589			
VERSION	AR073589.1	GI:10000353		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 559)			
TITLE	Yue, H., Corley N.C. and Shah, P.			
JOURNAL	DNA encoding a human progesterone receptor complex p23-like protein			
FEATURES	Patent: US 5952175-A 2 14-SEP-1999;			
	Location/Qualifiers			





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Db      385 CTGATGTGGAATATGACAGAGCTTTTGAAGAAGTGTGACGACCAAGAGAGCTCCACCTG 444
OY      421 CCATGGATGATTTGGAT 437
Db      445 CCATGGATGATTTGGAT 461

RESULT 5
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LOCUS    Homo sapiens cDNA FLJ32403 fls, clone SKMUS2000365, weakly similar
DEFINITION
ACCESSION AK056965
VERSION    AK056965.1 GI:16552512
KEYWORDS   oligo capping, fls (full insert sequence).
SOURCE      Homo sapiens skeletal muscle cDNA to mRNA, clone_11b:SKMUS2
             clone:SKMUS2000365.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS    1
            Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Matsushima,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
            Suzuki,Y., Sugano,S., Nagahari,K., Masuno,Y., Nagai,K. and
            Isogai,T.
TITLE       NEDO human cDNA sequencing project
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 1432)
AUTHORS     Isogai,T., Otsuki,T. and Sugiyama,T.
JOURNAL     Direct Submission
             Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
             Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
             (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
             NEDO human cDNA sequencing project supported by Ministry of
             Economy, Trade and Industry of Japan; cDNA full insert sequencing:
             Research Association for Biotechnology (RAB); cDNA library
             construction: Helix Research Institute (HRI) (supported by Japan
             Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
             HRI, and Biotechnology Center, National Institute of Technology and
             Evaluation; clone selection for full insert sequencing: RAB and
             HRI.

FEATURES
SOURCE      Location/Qualifiers
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             /clone_11b="SKMUS2"
             /note="cloning vector: PME18SFLJ3"

BASE COUNT 355 a 323 c 328 g 426 t

ORIGIN
Query Match 77.2%; Score 431.4; DB 9; Length 1432;
Best Local Similarity 99.8%; Pred. No. 1.3e-110;
Matches 432; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      127 GGTGAAGAATGCGCATGAGTGTGTACAAATGAGATTGAGTCTATGCGCAAGTGA 186
Db      39 GGTGAAGAATGCGCATGAGTGTGTACAAATGAGATTGAGTCTATGCGCAAGTGA 98

OY      187 ACTCCAAGAGACTCCAGATTAAGCGCTCTCCGCTCTATTACTTTGTTTGAGAAAT 246
Db      99 ACTCCAAGAGACTCCAGATTAAGCGCTCTCCGCTCTATTACTTTGTTTGAGAAAT 158

OY      247 GGAAGAAAAAGTGGCTGGCCGCGCTTACCAAGAGATATCAAGCCAGTGTGGCTGT 306
Db      159 GGAAGAAAAAGTGGCTGGCCGCGCTTACCAAGAGATATCAAGCCAGTGTGGCTGT 218

OY      307 CTGTGACTTTGATTAAGTGTGAGAGACTGGGAAGGGGATGAAGATGAGAGCTGGCTCATG 366

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Db      219 CTGTGACTTTGATTAAGTGTGAGAGACTGGGAAGGGGATGAAGATGAGAGCTGGCTCATG 278
OY      367 TCGAATATTATGACAGAGCTTTTGAAGAAGTGTGACGACCAAGAGAGCTCCACCTGCCATG 426
Db      279 TCGAATATTATGACAGAGCTTTTGAAGAAGTGTGACGACCAAGAGAGCTCCACCTGCCATG 338

OY      427 ATGATTGGATGATGATTTGTGACAGTGTGATGATCAACAGTATTACTTCTGTGA 486
Db      339 ATGATTGGATGATGATTTGTGACAGTGTGATGATCAACAGTATTACTTCTGTGA 398

OY      487 CGCAAGCTGGGAAGGACAGCTGTGCTATTTCACAGTTCTTCAAGAGTACGCGCTAG 546
Db      399 CGCAAGCTGGGAAGGACAGCTGTGCTATTTCACAGTTCTTCAAGAGTACGCGCTAG 458

OY      547 GCCTTTGTCAGCG 559
Db      459 GCCTTTGTCAGCG 471

RESULT 6
LOCUS    BC019324
DEFINITION
ACCESSION BC019324
VERSION    BC019324.1 GI:17939655
KEYWORDS   MGC.
SOURCE      Homo sapiens.
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS    1 (bases 1 to 1835)
JOURNAL     Strausberg,R.
JOURNAL     Direct Submission
             Submitted (13-DEC-2001) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA

REMARK     NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT     Contact: MGC help desk
             Email: cga@bbs-remail.nih.gov
             Tissue Procurement: DCTD/DP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
             DNA Sequencing by: Genome Sequence Centre,
             BC Cancer Agency, Vancouver, BC, Canada
             info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywicki, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Lung, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stolt,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAL Plate: 9 Row: p Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13376885.

FEATURES
SOURCE      Location/Qualifiers
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             /lab_host="DH10B-R"
             /note="Vector: pOTB7"

CDS
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 VEHIAELTKVSTRKPPAMDLDFTTTVVCSPAELQTEGNSNKKVLSGFQVLEDFD  
 TYLEPEGGGOPODRGTINDISLVLETRFGEADHPQTQPLDPSQVILVRYDMERFDB  
 MOGSHGLIAVADHLFKLTMTTWELGRFSALIELTPSTAQVAALIESVNEKIR  
 DRLVNVRKLSLDPEVEQVSGRLPDHADIPVAVIIPDSVNMCGTHVNSLSDLO  
 VIKLTIGREKGRKRNINLIFLSGNRVLMWESBSHTEKALFTLLCGAEDHVAVKILO  
 NSTIILGRNNINLRLDLVAHIAHLSRNSPDWGVVLIHRKGDSEFNMIIANEGSESE  
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 BASE COUNT 491 a 396 c 555 g 393 t  
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 Query Match 76.1%; Score 425.2; DB 9; Length 1835;  
 Best Local Similarity 99.3%; Pred. No. 7.4e-109;  
 Matches 427; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 GGCACGACGACGACGCCGCGACCTGTGGTACGACAGCCCATGTATGTTCATGAGAGTT 67  
 Db 94 GGGAAAGCAGCAGCGCCCGACCTGTGGTACGACAGCCCATGTATGTTCATGAGAGTT 153  
 QY 68 TTGTGTATGAGCAGCAGCACCAGTGTCCAGTGTCTTATTGAGATCAACCGCATTTGTTCAG 127  
 Db 154 TTGTGTATGAGCAGCAGCACCAGTGTCCAGTGTCTTATTGAGATCAACCGCATTTGTTCAG 213  
 QY 128 CTGCAAGATGCGCATGGAGTGGAGTGTGTACAAATGAGATGTGATTCATGCAAGTGAA 187  
 Db 214 CTGCAAGATGCGCATGGAGTGGAGTGTGTACAAATGAGATGTGATTCATGCAAGTGAA 273  
 QY 188 CTCCAAGAGCTCCCGAGATTAAGCGCTCTTCCGCTCTATTACTTTTGTGAGAAATG 247  
 Db 274 CTCCAAGAGCTCCCGAGATTAAGCGCTCTTCCGCTCTATTACTTTTGTGAGAAATG 333  
 QY 248 GAAAGAAAAAGTGGCGCTGGCGCGGCTTACCAAGAGAGATATCAAGCCAGTGTGGCTGTC 307  
 Db 334 GAAAGAAAAAGTGGCGCTGGCGCGGCTTACCAAGAGAGATATCAAGCCAGTGTGGCTGTC 393  
 QY 308 TGTGACATTTGTGTAAGTGGAGAGTGGGAAAGGGGATGAAAGATGGAAGCTGGCTCATGT 367  
 Db 394 TGTGACATTTGTGTAAGTGGAGAGTGGGAAAGGGGATGAAAGATGGAAGCTGGCTCATGT 453  
 QY 368 GGAACATTATGCAGAGCTTTTGAAGAGGTCAAGCAAGAGACCTCCACCTGTCATGGA 427  
 Db 454 GGAACATTATGCAGAGCTTTTGAAGAGGTCAAGCAAGAGACCTCCACCTGTCATGGA 513  
 QY 428 TGATTGGAT 437  
 Db 514 TGATTGGAT 523  
 RESULT 7  
 BC004172  
 LOCUS BC004172 1844 bp mRNA linear PRI 12-JUL-2001  
 DEFINITION Homo sapiens, clone MGC:2744 IMAGE:2823004, complete cds.  
 ACCESSION BC004172  
 VERSION BC004172.1 GI:13278806  
 KEYWORDS MGC.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1844)  
 AUTHORS Strausberg R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk  
 Email: gcaps-remail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: amadansystemsbiology.org  
 Anup Madan, Rachel Dickhoff, Jessica Fahney, Stephanie Ford, Julia  
 Greene, Mark Kelleman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnln.gov>  
 Series: IRAL Plate: 2 Row: f Column: 7.

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 NSRKTIQKNNLNLRLQVLVHLSLRNSPMGQVVLILHREGESEFNILLANEIGSEE  
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BASE COUNT	493 a	398 c	560 g	393 t
ORIGIN				
Query Match	76.1%	Score 425.2;	DB 9;	Length 1844;
Best Local Similarity	99.3%;	Pred. NO. 7.4e-109;		
Matches 427;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
8	GGCAGCGCAGACGCCCGCGACCTGTGTGATACAGACGCCCATGTATGTTCATGAGATT	67		
103	GGGAAGCGCAGACGCCCGCGACCTGTGTGTACGACAGGCCCATGATGTGTCATGAGATT	162		
68	TTGTGTGAGACAGACACCGATGTCACAGTCTTATTGAGATCACCGCATGTGTTTCAG	127		
163	TTGTGTGAGGACAGACACCGATGTCACAGTCTTATTGAGATCACCGCATGTGTTTCAG	222		
128	CTGCAAGATATCCGATGAGTGTGAGTGTACAAATGAGATTAGTTTATGCCAAAGTGA	187		
223	CTGCAAGATATCCGATGAGTGTGAGTGTACAAATGAGATTAGTTTATGCCAAAGTGA	282		
188	CTCCAGAGATCCGATGAGTGTGAGTGTACAAATGAGATTAGTTTATGCCAAAGTGA	247		
283	CTCCAGAGATCCGATGAGTGTGAGTGTACAAATGAGATTAGTTTATGCCAAAGTGA	342		
248	GAAGGAAAGGTGGCTTGGCGGGCTTACCAAGGAGATATCAAGCATGATGGCTGTC	307		
343	GAAGGAAAGGTGGCTTGGCGGGCTTACCAAGGAGATATCAAGCATGATGGCTGTC	402		
308	TGTGACTTTGATTAAGTGTGAGACTGTGGAAGGGGATGAAGATGAGCTGAGCTCATGT	367		
403	TGTGACTTTGATTAAGTGTGAGACTGTGGAAGGGGATGAAGATGAGCTGAGCTCATGT	462		
368	GGACATTATGACAGAGCTTTTGAAGAAGGTGACGACCAAGAGACTGCACCTGCCATGGA	427		
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OY 428 TGATTGAT 437  
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 DB 523 TGATTGAT 532

**RESULT 8**  
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 LOCUS AC046171  
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 HTG: HTGS\_PHASE1, HTGS\_DRAFT.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 189149)  
 Birren, B., Linton, L., Nusbaum, C., and Lander, E.  
 Homo sapiens chromosome 17, clone RP11-948G15  
 Unpublished  
 2 (bases 1 to 189149)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,  
 Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,  
 Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,  
 Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.,  
 Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,  
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
 Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,  
 Howland, J., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
 Klein, J., Lacroque, K., Lamazares, R., Landers, T., Lehoczeky, J.,  
 Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,  
 McCarthy, M., McEwan, P., McGurk, A., McKernan, R., McPheters, R.,  
 Melarini, J., Meneses, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,  
 Murphy, T., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Olivar, T., Oliver, J., Peterson, K., Pierre, N.,  
 Pisanic, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rotman, D.,  
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Testafaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,  
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wymann, D., Ye, W., J.,  
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (13-APR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 2, 2001 this sequence version replaced g1:7712190.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence.submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L7946  
 Center clone name: 948\_G\_15  
 ----- Summary Statistics  
 Sequencing vector: M13; M77815; 40% of reads  
 Sequencing vector: Plasmid; n/a; 60% of reads  
 Chemistry: Dye-terminator Big Dye, 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 185448 bases at least Q40  
 Consensus quality: 186995 bases at least Q30  
 Consensus quality: 187536 bases at least Q20  
 Insert size: 190000; agarose-efp  
 Insert size: 187849; sum-of-contigs  
 Quality coverage: 10.0 in Q20 bases; agarose-efp  
 Quality coverage: 10.1 in Q20.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 14 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1116: contig of 1116 bp in length  
 \* 1117 1126: gap of 100 bp  
 \* 1127 13252: contig of 2036 bp in length  
 \* 13253 13352: gap of 100 bp  
 \* 13353 16335: contig of 3183 bp in length  
 \* 16336 16635: gap of 100 bp  
 \* 16636 20967: contig of 4332 bp in length  
 \* 20968 21067: gap of 100 bp  
 \* 21068 24711: contig of 3644 bp in length  
 \* 24712 24811: gap of 100 bp  
 \* 24812 52351: contig of 27540 bp in length  
 \* 52352 52451: gap of 100 bp  
 \* 52452 62074: contig of 9623 bp in length  
 \* 62075 62174: gap of 100 bp  
 \* 62175 70797: contig of 8623 bp in length  
 \* 70798 70897: gap of 100 bp  
 \* 70898 92634: contig of 21737 bp in length  
 \* 92635 92734: gap of 100 bp  
 \* 92735 106944: contig of 14210 bp in length  
 \* 106945 107044: gap of 100 bp  
 \* 107045 129146: contig of 22102 bp in length  
 \* 129147 129246: gap of 100 bp  
 \* 129247 157583: contig of 28337 bp in length  
 \* 157584 157683: gap of 100 bp  
 \* 157684 183142: contig of 25459 bp in length  
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BASE COUNT 50053 a 45663 c 44537 g 47593 t 1303 others





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LOCUS Homo sapiens chromosome 17 clone RP11-948G15 map 17, WORKING DRAFT  
DEFINITION  
AC046171.3 GI:13184209  
AC046171.3  
SEQUENCE 14 unordered pieces.  
HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
VERSION  
AC046171.3  
KEYWORDS  
HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE  
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ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 189149) Nussbaum, C. and Lander, E.  
Birren, B., Linton, L., Nussbaum, C. and Lander, E.  
Homo sapiens chromosome 17, clone RP11-948G15  
Unpublished  
2 (bases 1 to 189149)  
Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,  
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,  
Campiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,  
Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,  
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Testafaye, S., Theodore, J., Turrelli, A., Travers, M., Triggillo, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (13-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 2, 2001 this sequence version replaced gi:7712190.  
All repeats were identified using RepeatMasker:  
Smith, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WTR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L7946  
Center clone name: 948.G.15  
----- Summary Statistics  
Sequencing vector: M13; M77815; 40% of reads  
Sequencing vector: Plasmid; n/a; 60% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 185448 bases at least Q40  
Consensus quality: 186995 bases at least Q30  
Consensus quality: 187536 bases at least Q20  
Insert size: 190000; agarose-fp  
Insert size: 187849; sum-of-contigs  
Quality coverage: 10.0 in Q20 bases; agarose-fp  
Quality coverage: 10.1 in Q20.  
\* NOTE: This is a working draft sequence. It currently  
\* consists of 14 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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1	189149	20968	21067: gap of 100 bp
1	189149	21068	24711: contig of 3644 bp in length
1	189149	24712	24811: gap of 100 bp
1	189149	24812	52351: contig of 27540 bp in length
1	189149	52352	52451: gap of 100 bp
1	189149	52452	62074: contig of 9623 bp in length
1	189149	62075	62174: gap of 100 bp
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1	189149	70798	70897: gap of 100 bp
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 Db 45809 GGCACAGCCCCGACCTTGTGTAGACAGAGCCCATGTAATGTCATGAGATTGTCG 45868  
 Oy 73 TTGAGACAGACCCAGTGTCTACGTCTATTGAGATCAGCATTTGTGTACGCT 129  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 782)  
 AUTHORS Johnson,J.L., Belto,T.G., Krcso,C.J. and Toft,D.O.  
 TITLE Characterization of a novel 23-kilodalton protein of inactive  
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 JOURNAL Mol. Cell. Biol. 14 (3), 1956-1963 (1994)  
 MEDLINE 94158868  
 PUBMED 8114727  
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 Matches 220; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

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 Oy 121 TGTTCAGCTGAGAAATGCC---GATGAGTGTGATGATGATGATGATGATG 177  
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 Oy 178 CCMAAGTGAATCCCAAGAGACTCCAGATAGCGCTTCCCGCTCTATTACTTGTG 237  
 Db 402 ACTGATTTGATCCAAATGATTCAGAGCAATAAAGAGACAGATCAATTTATGTTG 461  
 Oy 238 TGAGAAATGGAAGAAAGGTGGCCCTGGCCGCTTACCAAGAGGATATCAAGCCAG 297  
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 Oy 298 TGTGCTGTCTGTGACCTTGTGATCTGAGAGACTGGAGAAAGGATGAAGATGAGAC 357

Db 522 ATTGGCTAGTGTGCACTTCAATTAATTGGAAGACTGGAGAGATGATGATGAGAGACA 581  
 Oy 358 TGGCTCATGTGGAACATTAATGACAGAGCTTTTGAGAGA 394  
 Db 582 TGTCTAATTTGATCGCTTCTCTGAGATGATGAGAACAA 618  
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 DEFINITION Homo sapiens, inactive progesterone receptor, 23 kd, clone MGC:4004  
 IMAGE:2821965, mRNA, complete cds.  
 ACCESSION BC003005  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1490)  
 AUTHORS Strausberg,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-FEB-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 CONTACT: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: DCTP/DMP  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
 info@bcgsc.bc.ca  
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
 Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
 Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McEavey, Steven  
 Ness, Pawan Pandoh, Anna-Lisa Parvaneh, Parvaneh Saeedi, Jacqueline  
 Schein, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Stott,  
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
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 Best Local Similarity 54.1%; Pred. No. 5.1e-18;



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

fragments are separated by dashed lines.

ECORI	HindIII	BglIII
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fragments are separated by dashed lines.

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ECORI	HindIII	BglII
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486	<800	2814	2848	2638	2680
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6378	6427	4695	4691	200	<800
307	<800	3373	3417	2223	2254
681	<800	5553	5549	11143	11078
2173	2176	2961	3007	421	<800
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Best Local Similarity	53.9%; Pred. No. 2.3e-17;
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DB 29738	TTGAATTTTGTGTGTAAGACGATGATTAATTTTAAATCCAAACTTA 29679
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DB 29618	ACTGATTGATTCACAAAGCATTCGAAGCATTAAGAAAGACGACATCAATTTATGTTT 29559
QY 238	TGAGAAATGAGAGAAAAGTGCGCTGCGCCGCTTACCAAGAGGATATCAAGCCAG 297
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QY 298	TGTGCTGTCTGTGACTTTGATTAAGTGAAGAGAGATGGAAGGATGAGATGAGAC 357
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